

GENERAL PATHWAY OF LIGNIN BIOSYNTHESIS

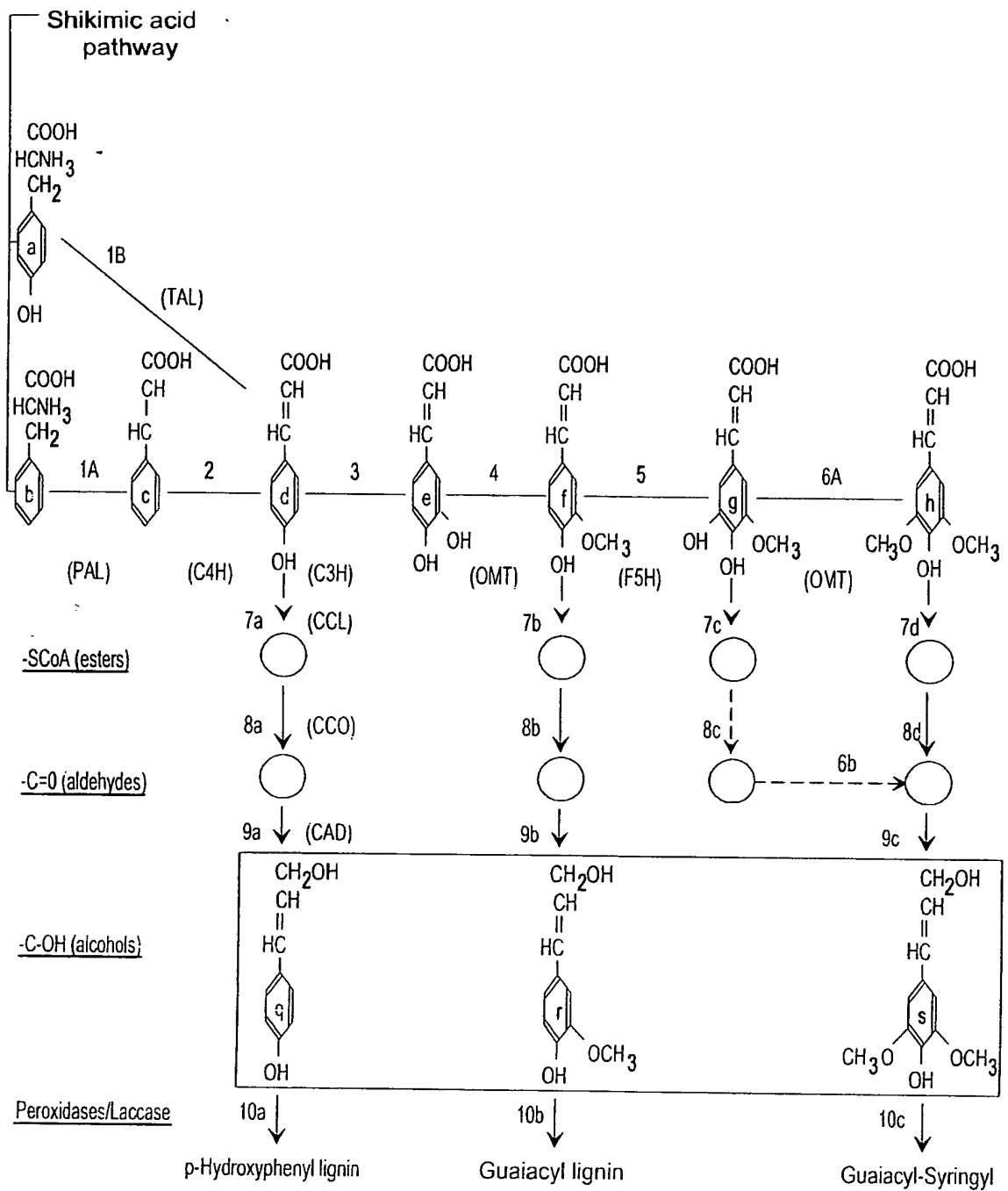


FIG. 1

SEQ ID 5

<400> 5

cggcacgagc cctacctcct ttcttgga aaatttcccca ttcgatcaca atccgggcct 60

caaaaa atg gga tca aca agc gaa acg aag atg agc ccg agt gaa gca 108
Met Gly Ser Thr Ser Glu Thr Lys Met Ser Pro Ser Glu Ala

1 5 10

gca gca gca gaa gaa gaa gca ttc gta ttc gct atg caa tta acc agt 156
Ala Ala Ala Glu Glu Glu Ala Phe Val Phe Ala Met Gln Leu Thr Ser
15 20 25 30

gct tca gtt ctt ccc atg gtc cta aaa tca gcc ata gag ctc gac gtc 204
Ala Ser Val Leu Pro Met Val Leu Lys Ser Ala Ile Glu Leu Asp Val
35 40 45

tta gaa atc atg gct aaa gct ggt cca ggt gcg cac ata tcc aca tct 252
Leu Glu Ile Met Ala Lys Ala Gly Pro Gly Ala His Ile Ser Thr Ser
50 55 60

gac ata gcc tct aag ctg ccc aca aag aat cca gat gca gcc gtc atg 300
Asp Ile Ala Ser Lys Leu Pro Thr Lys Asn Pro Asp Ala Ala Val Met
65 70 75

ctt gac cgt atg ctc cgc ctc ttg gct agc tac tct gtt cta acg tgc 348
Leu Asp Arg Met Leu Arg Leu Leu Ala Ser Tyr Ser Val Leu Thr Cys
80 85 90

tct ctc cgc acc ctc cct gac ggc aag atc gag agg ctt tac ggc ctt 396
Ser Leu Arg Thr Leu Pro Asp Gly Lys Ile Glu Arg Leu Tyr Gly Leu
95 100 105 110

gca ccc gtt tgt aaa ttc ttg acc aga aac gat gat gga gtc tcc ata 444
Ala Pro Val Cys Lys Phe Leu Thr Arg Asn Asp Asp Gly Val Ser Ile
115 120 125

gcc gct ctg tct ctc atg aat caa gac aag gtc ctc atg gag agc tgg 492
Ala Ala Leu Ser Leu Met Asn Gln Asp Lys Val Leu Met Glu Ser Trp
130 135 140

tac cac ttg acc gag gca gtt ctt gaa ggt gga att cca ttt aac aag 540
Tyr His Leu Thr Glu Ala Val Leu Glu Gly Gly Ile Pro Phe Asn Lys

145 150 155

Fig. 2A

SEQ ID 5

gcc tat gga atg aca gca ttt gag tac cat ggc acc gat ccc aga ttc	588
Ala Tyr Gly Met Thr Ala Phe Glu Tyr His Gly Thr Asp Pro Arg Phe	
160 165 170	
aac aca gtt ttc aac aat gga atg tcc aat cat tcg acc att acc atg	636
Asn Thr Val Phe Asn Asn Gly Met Ser Asn His Ser Thr Ile Thr Met	
175 180 185 190	
aag aaa atc ctt gag act tac aaa ggg ttc gag gga ctt gga tct gtg	684
Lys Lys Ile Leu Glu Thr Tyr Lys Gly Phe Glu Gly Leu Gly Ser Val	
195 200 205	
gtt gat gtt ggt ggt ggc act ggt gcc cac ctt aac atg att atc gct	732
Val Asp Val Gly Gly Gly Thr Gly Ala His Leu Asn Met Ile Ile Ala	
210 215 220	
aaa tac ccc atg atc aag ggc att aac ttc gac ttg cct cat gtt att	780
Lys Tyr Pro Met Ile Lys Gly Ile Asn Phe Asp Leu Pro His Val Ile	
225 230 235	
gag gag gct ccc tcc tat cct ggt gtg gag cat gtt ggt gga gat atg	828
Glu Glu Ala Pro Ser Tyr Pro Gly Val Glu His Val Gly Gly Asp Met	
240 245 250	
ttt gtt agt gtt cca aaa gga gat gcc att ttc atg aag tgg ata tgt	876
Phe Val Ser Val Pro Lys Gly Asp Ala Ile Phe Met Lys Trp Ile Cys	
255 260 265 270	
cat gat tgg agc gat gaa cac tgc ttg aag ttt ttg aag aaa tgt tat	924
His Asp Trp Ser Asp Glu His Cys Leu Lys Phe Leu Lys Lys Cys Tyr	
275 280 285	
gaa gca ctt cca acc aat ggg aag gtg atc ctt gct gaa tgc atc ctc	972
Glu Ala Leu Pro Thr Asn Gly Lys Val Ile Leu Ala Glu Cys Ile Leu	
290 295 300	
ccc gtg gcg cca gac gca agc ctc ccc act aag gca gtg gtc cat att	1020
Pro Val Ala Pro Asp Ala Ser Leu Pro Thr Lys Ala Val Val His Ile	
305 310 315	
gat gtc atc atg ttg gct cat aac cca ggt ggg aaa gag aga act gag	1068
Asp Val Ile Met Leu Ala His Asn Pro Gly Gly Lys Glu Arg Thr Glu	
320 325 330	
aag gag ttt gag gcc ttg gcc aag ggg gct gga ttt gaa ggt ttc cga	1116
Lys Glu Phe Glu Ala Leu Ala Lys Gly Ala Gly Phe Glu Gly Phe Arg	

Fig. 2B

SEQ ID 5

335		340		345		350	
gta gta gcc tcg tgc gct tac aat aca tgg atc atc gaa ttt ttg aag	1164						
Val Val Ala Ser Cys Ala Tyr Asn Thr Trp Ile Ile Glu Phe Leu Lys							
		355		360		365	
aag att tgagtcctta ctcggtttg agtacataat accaactcct tttggttttc	1220						
Lys Ile							
gagattgtga ttgtgattgt gattgtctct ctttcgcagt tggccttatg atataatgta	1280						
tcgttaactc gatcacagaa gtgcaaaaga cagtgaatgt aactgcttt ataaaataaa	1340						
aattttaaga ttttgattca tgtaaaaaaa aaaaaaaaaa	1380						

Fig. 2C

SEQ ID 6

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<400> 6
Met Gly Ser Thr Ser Glu Thr Lys Met Ser Pro Ser Glu Ala Ala Ala
 1           5           10           15

Ala Glu Glu Glu Ala Phe Val Phe Ala Met Gln Leu Thr Ser Ala Ser
      20           25           30

Val Leu Pro Met Val Leu Lys Ser Ala Ile Glu Leu Asp Val Leu Glu
      35           40           45

Ile Met Ala Lys Ala Gly Pro Gly Ala His Ile Ser Thr Ser Asp Ile
      50           55           60

Ala Ser Lys Leu Pro Thr Lys Asn Pro Asp Ala Ala Val Met Leu Asp
      65           70           75           80

Arg Met Leu Arg Leu Leu Ala Ser Tyr Ser Val Leu Thr Cys Ser Leu
      85           90           95

Arg Thr Leu Pro Asp Gly Lys Ile Glu Arg Leu Tyr Gly Leu Ala Pro
      100          105          110

Val Cys Lys Phe Leu Thr Arg Asn Asp Asp Gly Val Ser Ile Ala Ala
      115          120          125

Leu Ser Leu Met Asn Gln Asp Lys Val Leu Met Glu Ser Trp Tyr His
      130          135          140

Leu Thr Glu Ala Val Leu Glu Gly Gly Ile Pro Phe Asn Lys Ala Tyr
      145          150          155          160

Gly Met Thr Ala Phe Glu Tyr His Gly Thr Asp Pro Arg Phe Asn Thr
      165          170          175

Val Phe Asn Asn Gly Met Ser Asn His Ser Thr Ile Thr Met Lys Lys
      180          185          190

Ile Leu Glu Thr Tyr Lys Gly Phe Glu Gly Leu Gly Ser Val Val Asp
      195          200          205

Val Gly Gly Gly Thr Gly Ala His Leu Asn Met Ile Ile Ala Lys Tyr
      210          215          220

Pro Met Ile Lys Gly Ile Asn Phe Asp Leu Pro His Val Ile Glu Glu
      225          230          235          240

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Fig. 2D

SEQ ID 6

Ala	Pro	Ser	Tyr	Pro	Gly	Val	Glu	His	Val	Gly	Gly	Asp	Met	Phe	Val			
				245					250					255				
Ser	Val	Pro	Lys	Gly	Asp	Ala	Ile	Phe	Met	Lys	Trp	Ile	Cys	His	Asp			
			260					265					270					
Trp	Ser	Asp	Glu	His	Cys	Leu	Lys	Phe	Leu	Lys	Lys	Cys	Tyr	Glu	Ala			
		275					280					285						
Leu	Pro	Thr	Asn	Gly	Lys	Val	Ile	Leu	Ala	Glu	Cys	Ile	Leu	Pro	Val			
	290					295					300							
Ala	Pro	Asp	Ala	Ser	Leu	Pro	Thr	Lys	Ala	Val	Val	His	Ile	Asp	Val			
305					310				315					320				
Ile	Met	Leu	Ala	His	Asn	Pro	Gly	Gly	Lys	Glu	Arg	Thr	Glu	Lys	Glu			
				325				330						335				
Phe	Glu	Ala	Leu	Ala	Lys	Gly	Ala	Gly	Phe	Glu	Gly	Phe	Arg	Val	Val			
		340					345					350						
Ala	Ser	Cys	Ala	Tyr	Asn	Thr	Trp	Ile	Ile	Glu	Phe	Leu	Lys	Lys	Ile			
		355				360					365							

Fig. 2E

SEQ ID 7

<400> 7

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cggcacgagc tcattttcca cttctggttt gatctctgca attcttccat cagtcacct 59

atg gag acc caa aca aaa caa gaa gaa atc ata tat cgg tcg aaa ctc 107
Met Glu Thr Gln Thr Lys Gln Glu Glu Ile Ile Tyr Arg Ser Lys Leu
  1           5           10           15

ccc gat atc tac atc ccc aaa cac ctc cct tta cat tcg tat tgt ttc 155
Pro Asp Ile Tyr Ile Pro Lys His Leu Pro Leu His Ser Tyr Cys Phe
          20           25           30

gag aac atc tca cag ttc ggc tcc cgc ccc tgt ctg atc aat ggc gca 203
Glu Asn Ile Ser Gln Phe Gly Ser Arg Pro Cys Leu Ile Asn Gly Ala
          35           40           45

acg ggc aag tat tac aca tat gct gag gtt gag ctc att gcg cgc aag 251
Thr Gly Lys Tyr Tyr Thr Tyr Ala Glu Val Glu Leu Ile Ala Arg Lys
          50           55           60

gtc gca tcc ggc ctc aac aaa ctc ggc gtt cga caa ggt gac atc atc 299
Val Ala Ser Gly Leu Asn Lys Leu Gly Val Arg Gln Gly Asp Ile Ile
          65           70           75           80

atg ctt ttg cta ccc aac tcg ccg gag ttc gtg ttt tca att ctc ggc 347
Met Leu Leu Leu Pro Asn Ser Pro Glu Phe Val Phe Ser Ile Leu Gly
          85           90           95

gca tcc tac cgc ggg gct gcc gcc acc gcc gca aac ccg ttt tat acc 395
Ala Ser Tyr Arg Gly Ala Ala Ala Thr Ala Ala Asn Pro Phe Tyr Thr
          100           105           110

cct gcc gag atc agg aag caa gcc aaa acc tcc aac gcc agg ctt att 443
Pro Ala Glu Ile Arg Lys Gln Ala Lys Thr Ser Asn Ala Arg Leu Ile
          115           120           125

atc aca cat gcc tgt tac tat gag aaa gtg aag gac ttg gtg gaa gag 491
Ile Thr His Ala Cys Tyr Tyr Glu Lys Val Lys Asp Leu Val Glu Glu
          130           135           140

aac gtt gcc aag atc ata tgt ata gac tca ccc ccg gac ggt tgt ttg 539
Asn Val Ala Lys Ile Ile Cys Ile Asp Ser Pro Pro Asp Gly Cys Leu
          145           150           155           160

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Fig. 3A

SEQ ID 7

cac ttc tcg gcg ctg agt gag gcg gac gag aac gac atg ccc aat gta	587
His Phe Ser Glu Leu Ser Glu Ala Asp Glu Asn Asp Met Pro Asn Val	
165 170 175	
gag att gac ccc gat gat gtg gtg gcg ctg ccg tac tcg tca ggg acg	635
Glu Ile Asp Pro Asp Asp Val Val Ala Leu Pro Tyr Ser Ser Gly Thr	
180 185 190	
acg ggt tta cca aag ggg gtg atg cta aca cac aag gga caa gtg acg	683
Thr Gly Leu Pro Lys Gly Val Met Leu Thr His Lys Gly Gln Val Thr	
195 200 205	
agt gtg gcg caa cag gtg gac gga gag aat ccg aac ctg tat ata cat	731
Ser Val Ala Gln Gln Val Asp Gly Glu Asn Pro Asn Leu Tyr Ile His	
210 215 220	
agc gag gac gtg gtt ctg tgc gtg ttg cct ctg ttt cac atc tac tcg	779
Ser Glu Asp Val Val Leu Cys Val Leu Pro Leu Phe His Ile Tyr Ser	
225 230 235 240	
atg aac gtc atg ttt tgc ggg tta cga gtt ggt gcg gcg att ctg att	827
Met Asn Val Met Phe Cys Gly Leu Arg Val Gly Ala Ala Ile Leu Ile	
245 250 255	
atg cag aaa ttt gaa ata tat ggg ttg tta gag ctg gtc aga agt aca	875
Met Gln Lys Phe Glu Ile Tyr Gly Leu Leu Glu Leu Val Arg Ser Thr	
260 265 270	
ggt gac cat cat gcc tat cgt aca ccc atc gta ttg gca atc tcc aag	923
Gly Asp His His Ala Tyr Arg Thr Pro Ile Val Leu Ala Ile Ser Lys	
275 280 285	
act ccg gat ctt cac aac tat gat gtg tcc tcc att cgg act gtc atg	971
Thr Pro Asp Leu His Asn Tyr Asp Val Ser Ser Ile Arg Thr Val Met	
290 295 300	
tca ggt gcg gct cct ctg ggc aag gaa ctt gaa gat tct gtc aga gct	1019
Ser Gly Ala Ala Pro Leu Gly Lys Glu Leu Glu Asp Ser Val Arg Ala	
305 310 315 320	
aag ttt ccc acc gcc aaa ctt ggt cag gga tat gga atg acg gag gca	1067
Lys Phe Pro Thr Ala Lys Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala	
325 330 335	
ggg ccc gtg cta gcg atg tgt ttg gca ttt gcc aag gaa ggg ttt gaa	1115
Gly Pro Val Leu Ala Met Cys Leu Ala Phe Ala Lys Glu Gly Phe Glu	
340 345 350	

Fig. 3B

SEQ ID 7

ata aaa tcg ggg gca tct gga act gtt tta agy aac gca cag atg aag	1163
Ile Lys Ser Gly Ala Ser Gly Thr Val Leu Arg Asn Ala Gln Met Lys	
355 360 365	
att gtg gac cct gaa acc ggt gtc act ctc cct cga aac caa ccc gga	1211
Ile Val Asp Pro Glu Thr Gly Val Thr Leu Pro Arg Asn Gln Pro Gly	
370 375 380	
gag att tgc att aga gga gac caa atc atg aaa ggt tat ctt aat gat	1259
Glu Ile Cys Ile Arg Gly Asp Gln Ile Met Lys Gly Tyr Leu Asn Asp	
385 390 395 400	
cct gag gcg acg gag aga acc ata gac aag gaa ggt tgg tta cac aca	1307
Pro Glu Ala Thr Glu Arg Thr Ile Asp Lys Glu Gly Trp Leu His Thr	
405 410 415	
ggt gat gtg ggc tac atc gac gat gac act gag ctc ttc att gtt gat	1355
Gly Asp Val Gly Tyr Ile Asp Asp Asp Thr Glu Leu Phe Ile Val Asp	
420 425 430	
cgg ttg aag gaa ctg atc aaa tac aaa ggg ttt cag gtg gca ccc gct	1403
Arg Leu Lys Glu Leu Ile Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala	
435 440 445	
gag ctt gag gcc atg ctc ctc aac cat ccc aac atc tct gat gct gcc	1451
Glu Leu Glu Ala Met Leu Leu Asn His Pro Asn Ile Ser Asp Ala Ala	
450 455 460	
gtc gtc cca atg aaa gac gat gaa gct gga gag ctc cct gtg gcg ttt	1499
Val Val Pro Met Lys Asp Asp Glu Ala Gly Glu Leu Pro Val Ala Phe	
465 470 475 480	
gtt gta aga tca gat ggt tct cag ata tcc gag gct gaa atc agg caa	1547
Val Val Arg Ser Asp Gly Ser Gln Ile Ser Glu Ala Glu Ile Arg Gln	
485 490 495	
tac atc gca aaa cag gtg gtt ttt tat aaa aga ata cat cgc gta ttt	1595
Tyr Ile Ala Lys Gln Val Val Phe Tyr Lys Arg Ile His Arg Val Phe	
500 505 510	
ttc gtc gaa gcc att cct aaa gcg ccc tct ggc aaa atc ttg cgg aag	1643
Phe Val Glu Ala Ile Pro Lys Ala Pro Ser Gly Lys Ile Leu Arg Lys	
515 520 525	
gac ctg aga gcc aaa ttg gcg tct ggt ctt ccc aat taattctcat	1689
Asp Leu Arg Ala Lys Leu Ala Ser Gly Leu Pro Asn	
530 535 540	

Fig. 3C

SEQ ID 7

tcgctaccct cctttctctt atcatacgcc aacacgaacg aagaggctca attaaacgct 1749
gctcattcga agcggctcaa tttaaagctgc tcattcatgt ccaccgagtg ggcagcctgt 1809
cttgttggga tgttctttca tttgattcag ctgtgagaag ccagaccctc attattttatt 1869
gtgaaattca caagaatgct tgtaaatacga tgttgtagt gatgggtttc aaaacacttt 1929
tgacattgtt tacgttgtat ttctgtctgt tgaaaataac tactttgtat gactttttatt 1989
tggaagata acctttcaaa aaaaaaaaaa aaaaaa 2025

Fig. 3D

SEQ ID 8

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<400> 8
Met Glu Thr Gln Thr Lys Gln Glu Glu Ile Ile Tyr Arg Ser Lys Leu
  1              5              10              15

Pro Asp Ile Tyr Ile Pro Lys His Leu Pro Leu His Ser Tyr Cys Phe
      20              25              30

Glu Asn Ile Ser Gln Phe Gly Ser Arg Pro Cys Leu Ile Asn Gly Ala
      35              40              45

Thr Gly Lys Tyr Tyr Thr Tyr Ala Glu Val Glu Leu Ile Ala Arg Lys
      50              55              60

Val Ala Ser Gly Leu Asn Lys Leu Gly Val Arg Gln Gly Asp Ile Ile
      65              70              75              80

Met Leu Leu Leu Pro Asn Ser Pro Glu Phe Val Phe Ser Ile Leu Gly
      85              90              95

Ala Ser Tyr Arg Gly Ala Ala Ala Thr Ala Ala Asn Pro Phe Tyr Thr
      100             105             110

Pro Ala Glu Ile Arg Lys Gln Ala Lys Thr Ser Asn Ala Arg Leu Ile
      115             120             125

Ile Thr His Ala Cys Tyr Tyr Glu Lys Val Lys Asp Leu Val Glu Glu
      130             135             140

Asn Val Ala Lys Ile Ile Cys Ile Asp Ser Pro Pro Asp Gly Cys Leu
      145             150             155             160

His Phe Ser Glu Leu Ser Glu Ala Asp Glu Asn Asp Met Pro Asn Val
      165             170             175

Glu Ile Asp Pro Asp Asp Val Val Ala Leu Pro Tyr Ser Ser Gly Thr
      180             185             190

Thr Gly Leu Pro Lys Gly Val Met Leu Thr His Lys Gly Gln Val Thr
      195             200             205

Ser Val Ala Gln Gln Val Asp Gly Glu Asn Pro Asn Leu Tyr Ile His
      210             215             220

Ser Glu Asp Val Val Leu Cys Val Leu Pro Leu Phe His Ile Tyr Ser
      225             230             235             240

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Fig. 3E

SEQ ID 8

Met	Asn	Val	Met	Phe	Cys	Gly	Leu	Arg	Val	Gly	Ala	Ala	Ile	Leu	Ile			
				245					250					255				
Met	Gln	Lys	Phe	Glu	Ile	Tyr	Gly	Leu	Leu	Glu	Leu	Val	Arg	Ser	Thr			
			260					265					270					
Gly	Asp	His	His	Ala	Tyr	Arg	Thr	Pro	Ile	Val	Leu	Ala	Ile	Ser	Lys			
	275						280					285						
Thr	Pro	Asp	Leu	His	Asn	Tyr	Asp	Val	Ser	Ser	Ile	Arg	Thr	Val	Met			
	290					295					300							
Ser	Gly	Ala	Ala	Pro	Leu	Gly	Lys	Glu	Leu	Glu	Asp	Ser	Val	Arg	Ala			
305					310					315					320			
Lys	Phe	Pro	Thr	Ala	Lys	Leu	Gly	Gln	Gly	Tyr	Gly	Met	Thr	Glu	Ala			
				325					330					335				
Gly	Pro	Val	Leu	Ala	Met	Cys	Leu	Ala	Phe	Ala	Lys	Glu	Gly	Phe	Glu			
			340					345					350					
Ile	Lys	Ser	Gly	Ala	Ser	Gly	Thr	Val	Leu	Arg	Asn	Ala	Gln	Met	Lys			
	355						360					365						
Ile	Val	Asp	Pro	Glu	Thr	Gly	Val	Thr	Leu	Pro	Arg	Asn	Gln	Pro	Gly			
	370					375					380							
Glu	Ile	Cys	Ile	Arg	Gly	Asp	Gln	Ile	Met	Lys	Gly	Tyr	Leu	Asn	Asp			
385					390					395					400			
Pro	Glu	Ala	Thr	Glu	Arg	Thr	Ile	Asp	Lys	Glu	Gly	Trp	Leu	His	Thr			
				405					410					415				
Gly	Asp	Val	Gly	Tyr	Ile	Asp	Asp	Asp	Thr	Glu	Leu	Phe	Ile	Val	Asp			
			420					425					430					
Arg	Leu	Lys	Glu	Leu	Ile	Lys	Tyr	Lys	Gly	Phe	Gln	Val	Ala	Pro	Ala			
		435					440					445						
Glu	Leu	Glu	Ala	Met	Leu	Leu	Asn	His	Pro	Asn	Ile	Ser	Asp	Ala	Ala			
	450					455					460							
Val	Val	Pro	Met	Lys	Asp	Asp	Glu	Ala	Gly	Glu	Leu	Pro	Val	Ala	Phe			
465					470					475					480			

Fig. 3F

SEQ ID 8

Val	Val	Arg	Ser	Asp	Gly	Ser	Gln	Ile	Ser	Glu	Ala	Glu	Ile	Arg	Gln	
				485					490					495		
Tyr	Ile	Ala	Lys	Gln	Val	Val	Phe	Tyr	Lys	Arg	Ile	His	Arg	Val	Phe	
			500					505					510			
Phe	Val	Glu	Ala	Ile	Pro	Lys	Ala	Pro	Ser	Gly	Lys	Ile	Leu	Arg	Lys	
		515					520					525				
Asp	Leu	Arg	Ala	Lys	Leu	Ala	Ser	Gly	Leu	Pro	Asn					
	530					535					540					

Fig. 3G

SEQ ID 1

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cggcaccgagg aaaccctaaa actcacctct cttacccttt ctcttca atg gct ttc 56
                                     Met Ala Phe
                                     1

ctt cta ata ccc atc tca ata atc ttc atc gtc tta gct tac cag ctc 104
Leu Leu Ile Pro Ile Ser Ile Ile Phe Ile Val Leu Ala Tyr Gln Leu
    5      10      15

tat caa cgg ctc aga ttt aag ctc cca ccc ggc cca cgt cca tgg ccg 152
Tyr Gln Arg Leu Arg Phe Lys Leu Pro Pro Gly Pro Arg Pro Trp Pro
    20      25      30      35

atc gtc gga aac ctt tac gac ata aaa ccg gtg agg ttc cgg tgt ttc 200
Ile Val Gly Asn Leu Tyr Asp Ile Lys Pro Val Arg Phe Arg Cys Phe
    40      45      50

gcc gag tgg tca caa gcg tac ggt ccg atc ata tcg gtg tgg ttc ggt 248
Ala Glu Trp Ser Gln Ala Tyr Gly Pro Ile Ile Ser Val Trp Phe Gly
    55      60      65

tca acg ttg aat gtg atc gta tcg aat tcg gaa ttg gct aag gaa gtg 296
Ser Thr Leu Asn Val Ile Val Ser Asn Ser Glu Leu Ala Lys Glu Val
    70      75      80

ctc aag gaa aaa gat caa caa ttg gct gat agg cat agg agt aga tca 344
Leu Lys Glu Lys Asp Gln Gln Leu Ala Asp Arg His Arg Ser Arg Ser
    85      90      95

gct gcc aaa ttt agc agg gat ggg cag gac ctt ata tgg gct gat tat 392
Ala Ala Lys Phe Ser Arg Asp Gly Gln Asp Leu Ile Trp Ala Asp Tyr
    100      105      110      115

gga cct cac tat gtg aag gtt aca aag gtt tgt acc ctc gag ctt ttt 440
Gly Pro His Tyr Val Lys Val Thr Lys Val Cys Thr Leu Glu Leu Phe
    120      125      130

act cca aag cgg ctt gaa gct ctt aga ccc att aga gaa gat gaa gtt 488
Thr Pro Lys Arg Leu Glu Ala Leu Arg Pro Ile Arg Glu Asp Glu Val
    135      140      145

aca gcc atg gtt gag tcc att ttt aat gac act gcg aat cct gaa aat 536
Thr Ala Met Val Glu Ser Ile Phe Asn Asp Thr Ala Asn Pro Glu Asn
    150      155      160

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Fig. 4A

SEQ ID 1

tat ggg aag agt atg ctg gtg aag aag tat ttg gga gca gta gca ttc	584
Tyr Gly Lys Ser Met Leu Val Lys Lys Tyr Leu Gly Ala Val Ala Phe	
165 170 175	
aac aac att aca aga ctc gca ttt gga aag cga ttc gtg aat tca gag	632
Asn Asn Ile Thr Arg Leu Ala Phe Gly Lys Arg Phe Val Asn Ser Glu	
180 185 190 195	
ggt gta atg gac gag caa gga ctt gaa ttt aag gaa att gtg gcc aat	680
Gly Val Met Asp Glu Gln Gly Leu Glu Phe Lys Glu Ile Val Ala Asn	
200 205 210	
gga ctc aag ctt ggt gcc tca ctt gca atg gct gag cac att cct tgg	728
Gly Leu Lys Leu Gly Ala Ser Leu Ala Met Ala Glu His Ile Pro Trp	
215 220 225	
ctc cgt tgg atg ttc cca ctt gag gaa ggg gcc ttt gcc aag cat ggg	776
Leu Arg Trp Met Phe Pro Leu Glu Glu Gly Ala Phe Ala Lys His Gly	
230 235 240	
gca cgt agg gac cga ctt acc aga gct atc atg gaa gag cac aca ata	824
Ala Arg Arg Asp Arg Leu Thr Arg Ala Ile Met Glu Glu His Thr Ile	
245 250 255	
gcc cgt aaa aag agt ggt gga gcc caa caa cat ttc gtg gat gca ttg	872
Ala Arg Lys Lys Ser Gly Gly Ala Gln Gln His Phe Val Asp Ala Leu	
260 265 270 275	
ctc acc cta caa gag aaa tat gac ctt agc gag gac act att att ggg	920
Leu Thr Leu Gln Glu Lys Tyr Asp Leu Ser Glu Asp Thr Ile Ile Gly	
280 285 290	
ctc ctt tgg gat atg atc act gca ggc atg gac aca acc gca atc tct	968
Leu Leu Trp Asp Met Ile Thr Ala Gly Met Asp Thr Thr Ala Ile Ser	
295 300 305	
gtc gaa tgg gcc atg gcc gag tta att aag aac cca agg gtg caa caa	1016
Val Glu Trp Ala Met Ala Glu Leu Ile Lys Asn Pro Arg Val Gln Gln	
310 315 320	
aaa gct caa gag gag cta gac aat gta ctt ggg tcc gaa cgt gtc ctg	1064
Lys Ala Gln Glu Glu Leu Asp Asn Val Leu Gly Ser Glu Arg Val Leu	
325 330 335	

Fig. 4B

SEQ ID 1

acc gaa ttg gac ttc tca agc ctc cct tat cta caa tgt gta gcc aag	1112
Thr Glu Leu Asp Phe Ser Ser Leu Pro Tyr Leu Gln Cys Val Ala Lys	
340 345 350 355	
gag gca cta agg ctg cac cct cca aca cca cta atg ctc cct cat cgc	1160
Glu Ala Leu Arg Leu His Pro Pro Thr Pro Leu Met Leu Pro His Arg	
360 365 370	
gcc aat gcc aac gtc aaa att ggt ggc tac gac atc cct aag gga tca	1208
Ala Asn Ala Asn Val Lys Ile Gly Gly Tyr Asp Ile Pro Lys Gly Ser	
375 380 385	
aat gtt cat gta aat gtc tgg gcc gtg gct cgt gat cca gca gtg tgg	1256
Asn Val His Val Asn Val Trp Ala Val Ala Arg Asp Pro Ala Val Trp	
390 395 400	
cgt gac cca cta gag ttt cga ccg gaa cgg ttc tct gaa gac gat gtc	1304
Arg Asp Pro Leu Glu Phe Arg Pro Glu Arg Phe Ser Glu Asp Asp Val	
405 410 415	
gac atg aaa ggt cac gat tat agg cta ctg ccg ttt ggt gca ggg agg	1352
Asp Met Lys Gly His Asp Tyr Arg Leu Leu Pro Phe Gly Ala Gly Arg	
420 425 430 435	
cgt gtt tgc ccc ggt gca caa ctt ggc atc aat ttg gtc aca tcc atg	1400
Arg Val Cys Pro Gly Ala Gln Leu Gly Ile Asn Leu Val Thr Ser Met	
440 445 450	
atg ggt cac cta ttg cac cat ttc tat tgg agc cct cct aaa ggt gta	1448
Met Gly His Leu Leu His His Phe Tyr Trp Ser Pro Pro Lys Gly Val	
455 460 465	
aaa cca gag gag att gac atg tca gag aat cca gga ttg gtc acc tac	1496
Lys Pro Glu Glu Ile Asp Met Ser Glu Asn Pro Gly Leu Val Thr Tyr	
470 475 480	
atg cga acc ccg gtg caa gct gtt ccc act cca agg ctg cct gct cac	1544
Met Arg Thr Pro Val Gln Ala Val Pro Thr Pro Arg Leu Pro Ala His	
485 490 495	
ttg tac aaa cgt gta gct gtg gat atg taattcttag ttgttatta	1591
Leu Tyr Lys Arg Val Ala Val Asp Met	
500 505	

Fig. 4C

SEQ ID 1

ttcatgctct taaggttttg gactttgaac ttatgatgag atttgtaaaa ttccaagtga 1651
tcaaatgaag aaaagaccaa ataaaaaggc ttgacgattt aaaaaaaaaa aaaaaaa 1708

Fig. 4D

SEQ ID 2

Met	Ala	Phe	Leu	Leu	Ile	Pro	Ile	Ser	Ile	Ile	Phe	Ile	Val	Leu	Ala	1	5	10	15
Tyr	Gln	Leu	Tyr	Gln	Arg	Leu	Arg	Phe	Lys	Leu	Pro	Pro	Gly	Pro	Arg	20	25	30	
Pro	Trp	Pro	Ile	Val	Gly	Asn	Leu	Tyr	Asp	Ile	Lys	Pro	Val	Arg	Phe	35	40	45	
Arg	Cys	Phe	Ala	Glu	Trp	Ser	Gln	Ala	Tyr	Gly	Pro	Ile	Ile	Ser	Val	50	55	60	
Trp	Phe	Gly	Ser	Thr	Leu	Asn	Val	Ile	Val	Ser	Asn	Ser	Glu	Leu	Ala	65	70	75	80
Lys	Glu	Val	Leu	Lys	Glu	Lys	Asp	Gln	Gln	Leu	Ala	Asp	Arg	His	Arg	85	90	95	
Ser	Arg	Ser	Ala	Ala	Lys	Phe	Ser	Arg	Asp	Gly	Gln	Asp	Leu	Ile	Trp	100	105	110	
Ala	Asp	Tyr	Gly	Pro	His	Tyr	Val	Lys	Val	Thr	Lys	Val	Cys	Thr	Leu	115	120	125	
Glu	Leu	Phe	Thr	Pro	Lys	Arg	Leu	Glu	Ala	Leu	Arg	Pro	Ile	Arg	Glu	130	135	140	
Asp	Glu	Val	Thr	Ala	Met	Val	Glu	Ser	Ile	Phe	Asn	Asp	Thr	Ala	Asn	145	150	155	160
Pro	Glu	Asn	Tyr	Gly	Lys	Ser	Met	Leu	Val	Lys	Lys	Tyr	Leu	Gly	Ala	165	170	175	
Val	Ala	Phe	Asn	Asn	Ile	Thr	Arg	Leu	Ala	Phe	Gly	Lys	Arg	Phe	Val	180	185	190	
Asn	Ser	Glu	Gly	Val	Met	Asp	Glu	Gln	Gly	Leu	Glu	Phe	Lys	Glu	Ile	195	200	205	
Val	Ala	Asn	Gly	Leu	Lys	Leu	Gly	Ala	Ser	Leu	Ala	Met	Ala	Glu	His	210	215	220	
Ile	Pro	Trp	Leu	Arg	Trp	Met	Phe	Pro	Leu	Glu	Glu	Gly	Ala	Phe	Ala	225	230	235	240

Fig. 4E

SEQ ID 2

Lys	His	Gly	Ala	Arg	Arg	Asp	Arg	Leu	Thr	Arg	Ala	Ile	Met	Glu	Glu	245	250	255
His	Thr	Ile	Ala	Arg	Lys	Lys	Ser	Gly	Gly	Ala	Gln	Gln	His	Phe	Val	260	265	270
Asp	Ala	Leu	Leu	Thr	Leu	Gln	Glu	Lys	Tyr	Asp	Leu	Ser	Glu	Asp	Thr	275	280	285
Ile	Ile	Gly	Leu	Leu	Trp	Asp	Met	Ile	Thr	Ala	Gly	Met	Asp	Thr	Thr	290	295	300
Ala	Ile	Ser	Val	Glu	Trp	Ala	Met	Ala	Glu	Leu	Ile	Lys	Asn	Pro	Arg	305	310	315
Val	Gln	Gln	Lys	Ala	Gln	Glu	Glu	Leu	Asp	Asn	Val	Leu	Gly	Ser	Glu	325	330	335
Arg	Val	Leu	Thr	Glu	Leu	Asp	Phe	Ser	Ser	Leu	Pro	Tyr	Leu	Gln	Cys	340	345	350
Val	Ala	Lys	Glu	Ala	Leu	Arg	Leu	His	Pro	Pro	Thr	Pro	Leu	Met	Leu	355	360	365
Pro	His	Arg	Ala	Asn	Ala	Asn	Val	Lys	Ile	Gly	Gly	Tyr	Asp	Ile	Pro	370	375	380
Lys	Gly	Ser	Asn	Val	His	Val	Asn	Val	Trp	Ala	Val	Ala	Arg	Asp	Pro	385	390	395
Ala	Val	Trp	Arg	Asp	Pro	Leu	Glu	Phe	Arg	Pro	Glu	Arg	Phe	Ser	Glu	405	410	415
Asp	Asp	Val	Asp	Met	Lys	Gly	His	Asp	Tyr	Arg	Leu	Leu	Pro	Phe	Gly	420	425	430
Ala	Gly	Arg	Arg	Val	Cys	Pro	Gly	Ala	Gln	Leu	Gly	Ile	Asn	Leu	Val	435	440	445
Thr	Ser	Met	Met	Gly	His	Leu	Leu	His	His	Phe	Tyr	Trp	Ser	Pro	Pro	450	455	460
Lys	Gly	Val	Lys	Pro	Glu	Glu	Ile	Asp	Met	Ser	Glu	Asn	Pro	Gly	Leu	465	470	475
																		480

Fig. 4F

SEQ ID 2

Val Thr Tyr Met Arg Thr Pro Val Gln Ala Val Pro Thr Pro Arg Leu
485 490 495

Pro Ala His Leu Tyr Lys Arg Val Ala Val Asp Met
500 505

Fig. 4G

SEQ ID 3

<400> 3

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      Met Asp Ser Ser Leu His Glu Ala Leu Gln Pro Leu
            1                5                10

ccc atg acg ctg ttc ttc att ata cct ttg cta ctc tta ttg ggc cta      157
Pro Met Thr Leu Phe Phe Ile Ile Pro Leu Leu Leu Leu Leu Gly Leu
            15                20                25

gta tct cgg ctt cgc cag aga cta cca tac cca cca ggc cca aaa ggc      205
Val Ser Arg Leu Arg Gln Arg Leu Pro Tyr Pro Pro Gly Pro Lys Gly
            30                35                40

tta ccg gtg atc gga aac atg ctc atg atg gat caa ctc act cac cga      253
Leu Pro Val Ile Gly Asn Met Leu Met Met Asp Gln Leu Thr His Arg
            45                50                55                60

gga ctc gcc aaa ctc gcc aaa caa tac ggc ggt cta ttc cac ctc aag      301
Gly Leu Ala Lys Leu Ala Lys Gln Tyr Gln Gly Leu Phe His Leu Lys
            65                70                75

atg gga ttc tta cac atg gtg gcc gtt tcc aca ccc gac atg gct cgc      349
Met Gly Phe Leu His Met Val Ala Val Ser Thr Pro Asp Met Ala Arg
            80                85                90

caa gtc ctt caa gtc caa gac aac atc ttc tcg aac cgg cca gcc acc      397
Gln Val Leu Gln Val Gln Asp Asn Ile Phe Ser Asn Arg Pro Ala Thr
            95                100                105

ata gcc atc agc tac ctc acc tat gac cga gcc gac atg gcc ttc gct      445
Ile Ala Ile Ser Tyr Leu Thr Tyr Asp Arg Ala Asp Met Ala Phe Ala
            110                115                120

cac tac ggc ccg ttt tgg cgt cag atg cgt aaa ctc tgc gtc atg aaa      493
His Tyr Gly Pro Phe Trp Arg Gln Met Arg Lys Leu Cys Val Met Lys
            125                130                135                140

tta ttt agc cgg aaa cga gcc gag tcg tgg gag tcg gtc cga gac gag      541
Leu Phe Ser Arg Lys Arg Ala Glu Ser Trp Glu Ser Val Arg Asp Glu
            145                150                155

gtc gac tcg gca gta cga gtg gtc gcg tcc aat att ggg tcg acg gtg      589
Val Asp Ser Ala Val Arg Val Val Ala Ser Asn Ile Gly Ser Thr Val
            160                165                170

```

Fig. 5A

SEQ ID 3

aat atc ggc gag ctg gtt ttt gct ctg acg aag aat att act tac agg	637
Asn Ile Gly Glu Leu Val Phe Ala Leu Thr Lys Asn Ile Thr Tyr Arg	
175 180 185	
gcg gct ttt ggg acg atc tcg cat gag gac cag gac gag ttc gtg gcc	685
Ala Ala Phe Gly Thr Ile Ser His Glu Asp Gln Asp Glu Phe Val Ala	
190 195 200	
ata ctg caa gag ttt tcg cag ctg ttt ggt gct ttt aat ata gct gat	733
Ile Leu Gln Glu Phe Ser Gln Leu Phe Gly Ala Phe Asn Ile Ala Asp	
205 210 215 220	
ttt atc cct tgg ctc aaa tgg gtt cct cag ggg att aac gtc agg ctc	781
Phe Ile Pro Trp Leu Lys Trp Val Pro Gln Gly Ile Asn Val Arg Leu	
225 230 235	
aac aag gca cga ggg gcg ctt gat ggg ttt att gac aag atc atc gac	829
Asn Lys Ala Arg Gly Ala Leu Asp Gly Phe Ile Asp Lys Ile Ile Asp	
240 245 250	
gat cat ata cag aag ggg agt aaa aac tcg gag gag gtt gat act gat	877
Asp His Ile Gln Lys Gly Ser Lys Asn Ser Glu Glu Val Asp Thr Asp	
255 260 265	
atg gta gat gat tta ctt gct ttt tac ggt gag gaa gcc aaa gta agc	925
Met Val Asp Asp Leu Leu Ala Phe Tyr Gly Glu Glu Ala Lys Val Ser	
270 275 280	
gaa tct gac gat ctt caa aat tcc atc aaa ctc acc aaa gac aac atc	973
Glu Ser Asp Asp Leu Gln Asn Ser Ile Lys Leu Thr Lys Asp Asn Ile	
285 290 295 300	
aaa gct atc atg gac gta atg ttt gga ggg acc gaa acg gtg gcg tcc	1021
Lys Ala Ile Met Asp Val Met Phe Gly Gly Thr Glu Thr Val Ala Ser	
305 310 315	
gcg att gaa tgg gcc atg acg gag ctg atg aaa agc cca gaa gat cta	1069
Ala Ile Glu Trp Ala Met Thr Glu Leu Met Lys Ser Pro Glu Asp Leu	
320 325 330	
aag aag gtc caa caa gaa ctc gcc gtg gtg gtg ggt ctt gac cgg cga	1117
Lys Lys Val Gln Gln Glu Leu Ala Val Val Val Gly Leu Asp Arg Arg	
335 340 345	

Fig. 5B

SEQ ID 3

gtc gaa gag aaa gac ttc gag aag ctc acc tac ttg aaa tgc gta ctg	1165
Val Glu Glu Lys Asp Phe Glu Lys Leu Thr Tyr Leu Lys Cys Val Leu	
350 355 360	
aag gaa gtc ctt cgc ctc cac cca ccc atc cca ctc ctc ctc cac gag	1213
Lys Glu Val Leu Arg Leu His Pro Pro Ile Pro Leu Leu Leu His Glu	
365 370 375 380	
act gcc gag gac gcc gag gtc ggc ggc tac tac att ccg gcg aaa tcg	1261
Thr Ala Glu Asp Ala Glu Val Gly Gly Tyr Tyr Ile Pro Ala Lys Ser	
385 390 395	
cgg gtg atg atc aac gcg tgc gcc atc ggc cgg gac aag aac tcg tgg	1309
Arg Val Met Ile Asn Ala Cys Ala Ile Gly Arg Asp Lys Asn Ser Trp	
400 405 410	
gcc gac cca gat acg ttt agg ccc tcc agg ttt ctc aaa gac ggt gtg	1357
Ala Asp Pro Asp Thr Phe Arg Pro Ser Arg Phe Leu Lys Asp Gly Val	
415 420 425	
ccc gat ttc aaa ggg aac aac ttc gag ttc atc cca ttc ggg tca ggt	1405
Pro Asp Phe Lys Gly Asn Asn Phe Glu Phe Ile Pro Phe Gly Ser Gly	
430 435 440	
cgt cgg tct ttc ccc ggt atg caa ctc gga ctc tac gcg cta gag acg	1453
Arg Arg Ser Cys Pro Gly Met Gln Leu Gly Leu Tyr Ala Leu Glu Thr	
445 450 455 460	
act gtg gct cac ctc ctt cac tgt ttc acg tgg gag ttg ccg gac ggg	1501
Thr Val Ala His Leu Leu His Cys Phe Thr Trp Glu Leu Pro Asp Gly	
465 470 475	
atg aaa ccg agt gaa ctc gag atg aat gat gtg ttt gga ctc acc gcg	1549
Met Lys Pro Ser Glu Leu Glu Met Asn Asp Val Phe Gly Leu Thr Ala	
480 485 490	
cca aga gcg att cga ctc acc gcc gtg ccg agt cca cgc ctt ctc tgt	1597
Pro Arg Ala Ile Arg Leu Thr Ala Val Pro Ser Pro Arg Leu Leu Cys	
495 500 505	
cct ctc tat tgcacgaatg attgggggag ctttgtggag gggcttttat	1646
Pro Leu Tyr	
510	

Fig. 5C

SEQ ID 3

ggagactcta tatatagatg ggaagtgaaa caacgacagg tgaatgcttg gatttttggt 1706
atatattggg gagggagggg aaaaaaaaaa taatgaaagg aaagaaaga gagaatttga 1766
atttctcttc ctctgtggat aaaagcctcg tttttaattg ttttatgtg gagatatttg 1826
tgtttggtta ttttatctc tttttttgca ataacactca aaaataaaaa aaaaaa 1883

Fig. 5D

SEQ ID 4

<400> 4

Met	Asp	Ser	Ser	Leu	His	Glu	Ala	Leu	Gln	Pro	Leu	Pro	Met	Thr	Leu	1	5	10	15
Phe	Phe	Ile	Ile	Pro	Leu	Leu	Leu	Leu	Leu	Gly	Leu	Val	Ser	Arg	Leu	20	25	30	
Arg	Gln	Arg	Leu	Pro	Tyr	Pro	Pro	Gly	Pro	Lys	Gly	Leu	Pro	Val	Ile	35	40	45	
Gly	Asn	Met	Leu	Met	Met	Asp	Gln	Leu	Thr	His	Arg	Gly	Leu	Ala	Lys	50	55	60	
Leu	Ala	Lys	Gln	Tyr	Gly	Gly	Leu	Phe	His	Leu	Lys	Met	Gly	Phe	Leu	65	70	75	80
His	Met	Val	Ala	Val	Ser	Thr	Pro	Asp	Met	Ala	Arg	Gln	Val	Leu	Gln	85	90	95	
Val	Gln	Asp	Asn	Ile	Phe	Ser	Asn	Arg	Pro	Ala	Thr	Ile	Ala	Ile	Ser	100	105	110	
Tyr	Leu	Thr	Tyr	Asp	Arg	Ala	Asp	Met	Ala	Phe	Ala	His	Tyr	Gly	Pro	115	120	125	
Phe	Trp	Arg	Gln	Met	Arg	Lys	Leu	Cys	Val	Met	Lys	Leu	Phe	Ser	Arg	130	135	140	
Lys	Arg	Ala	Glu	Ser	Trp	Glu	Ser	Val	Arg	Asp	Glu	Val	Asp	Ser	Ala	145	150	155	160
Val	Arg	Val	Val	Ala	Ser	Asn	Ile	Gly	Ser	Thr	Val	Asn	Ile	Gly	Glu	165	170	175	
Leu	Val	Phe	Ala	Leu	Thr	Lys	Asn	Ile	Thr	Tyr	Arg	Ala	Ala	Phe	Gly	180	185	190	
Thr	Ile	Ser	His	Glu	Asp	Gln	Asp	Glu	Phe	Val	Ala	Ile	Leu	Gln	Glu	195	200	205	
Phe	Ser	Gln	Leu	Phe	Gly	Ala	Phe	Asn	Ile	Ala	Asp	Phe	Ile	Pro	Trp	210	215	220	
Leu	Lys	Trp	Val	Pro	Gln	Gly	Ile	Asn	Val	Arg	Leu	Asn	Lys	Ala	Arg	225	230	235	240

Fig. 5E

SEQ ID 4

Gly	Ala	Leu	Asp	Gly	Phe	Ile	Asp	Lys	Ile	Ile	Asp	Asp	His	Ile	Gln	245	250	255
Lys	Gly	Ser	Lys	Asn	Ser	Glu	Glu	Val	Asp	Thr	Asp	Met	Val	Asp	Asp	260	265	270
Leu	Leu	Ala	Phe	Tyr	Gly	Glu	Glu	Ala	Lys	Val	Ser	Glu	Ser	Asp	Asp	275	280	285
Leu	Gln	Asn	Ser	Ile	Lys	Leu	Thr	Lys	Asp	Asn	Ile	Lys	Ala	Ile	Met	290	295	300
Asp	Val	Met	Phe	Gly	Gly	Thr	Glu	Thr	Val	Ala	Ser	Ala	Ile	Glu	Trp	305	310	315
Ala	Met	Thr	Glu	Leu	Met	Lys	Ser	Pro	Glu	Asp	Leu	Lys	Lys	Val	Gln	325	330	335
Gln	Glu	Leu	Ala	Val	Val	Val	Gly	Leu	Asp	Arg	Arg	Val	Glu	Glu	Lys	340	345	350
Asp	Phe	Glu	Lys	Leu	Thr	Tyr	Leu	Lys	Cys	Val	Leu	Lys	Glu	Val	Leu	355	360	365
Arg	Leu	His	Pro	Pro	Ile	Pro	Leu	Leu	Leu	His	Glu	Thr	Ala	Glu	Asp	370	375	380
Ala	Glu	Val	Gly	Gly	Tyr	Tyr	Ile	Pro	Ala	Lys	Ser	Arg	Val	Met	Ile	385	390	395
Asn	Ala	Cys	Ala	Ile	Gly	Arg	Asp	Lys	Asn	Ser	Trp	Ala	Asp	Pro	Asp	405	410	415
Thr	Phe	Arg	Pro	Ser	Arg	Phe	Leu	Lys	Asp	Gly	Val	Pro	Asp	Phe	Lys	420	425	430
Gly	Asn	Asn	Phe	Glu	Phe	Ile	Pro	Phe	Gly	Ser	Gly	Arg	Arg	Ser	Cys	435	440	445
Pro	Gly	Met	Gln	Leu	Gly	Leu	Tyr	Ala	Leu	Glu	Thr	Thr	Val	Ala	His	450	455	460
Leu	Leu	His	Cys	Phe	Thr	Trp	Glu	Leu	Pro	Asp	Gly	Met	Lys	Pro	Ser	465	470	475

Fig. 5F

SEQ ID 4

Glu	Leu	Glu	Met	Asn	Asp	Val	Phe	Gly	Leu	Thr	Ala	Pro	Arg	Ala	Ile
			485						490					495	
Arg	Leu	Thr	Ala	Val	Pro	Ser	Pro	Arg	Leu	Leu	Cys	Pro	Leu	Tyr	
			500					505					510		

Fig. 5G

SEQ ID 10

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 ccgaaaacag cgaatgaaat gtctgggtga tcggtcaaac aagcgggtgg cgagagagcg 180
 cgggtgttgg cctagccggg atgggggtag gtagacggcg tattaccggc gagttgtccg 240
 aatggagttt tcggggtagg tagtaacgta gacgtcaatg gaaaaagtca taatctccgt 300
 caaaaatcca accgtcctt cacatcgag agttgggtggc cacgggaccc tccaccact 360
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Fig. 6

SEQ ID 11

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 aaaatattat acaaaattta ttaaaacttc aaaataaaca aactttttat acaaaattca 300
 tcaaaacttt aaaataaagc taaacactga aaatgtgagt acatttaaaa ggacgctgat 360
 cacaaaaatt ttgaaaacat aaacaaactt gaaactctac cttttaagaa tgagtttgtc 420
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 tggaaaaggt tggtaagaac tataaattga gttgtgaatg agtgttttat ggatttttta 660
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 caaaatcatt acattaaagc tcatcatgtc atttgtggat tggaaattat attgtataag 1260
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Fig. 7A

SEQ ID 11

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 taccaataa tatatttttt tatacatttt agagattttc cagacatatt tgctctggga 1500
 tttattggaa tgaagggtga gttataaact ttcagtaatc caagtatctt cggtttttga 1560
 agatactaaa tccattatat aataaaaaca cattttaaac accaatttaa tgggatttca 1620
 gatttgtatc ccatgctatt ggctaaggca tttttcttat tgtaattctaa ccaattctaa 1680
 tttccaccct ggtgtgaact gactgacaaa tgcggtccga aaacagcgaa tgaaatgtct 1740
 ggggtgatcg tcaaaacaagc ggtgggagag agagcgcggg tgttggccta gccgggatgg 1800
 gggtaggtag acggcgatatt accggcgagt tgtccgaatg gagttttcgg ggtaggtagt 1860
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 ccattattca accatacgcc acttgactct tcaccaacaa ttccaggccg gctttctata 2040
 caatgtactg cacaggaaaa tccaatataa aaagccggcc tctgcttctt tctcagtagc 2100
 cccagctca ttcaattctt cccactgcag gctacatttg tcagacacgt tttccgccaat 2160
 ttttcgctg tttctgcgga gaatttgatc aggttcggat tgggattgaa tcaattgaaa 2220
 ggtttttatt ttcagtattt cgatcgccat g 2251

Fig. 7B

SEQ ID 9

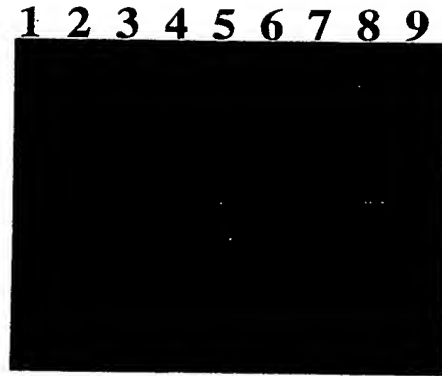
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aacgaaagaa acgtgtgtc accaactcgt gcactacatc ccgaaactta accttccct 420
gatacagatt gaagagccga aaaaagcgtg catccaaatt tctggtatgg tgaggagccg 480
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ttcacgtgtc gcgtattggc gaggttgcgc tgaatgtgat cctgtgcgtg agccacattc 600
attccattgg ttgaccgcc ggtaccgca ggaccgtggg gtctcacaga tacgcggatg 660
gtggatcagc actgagaaga ttagatgatg accaggcggg catttgaagt aaaaacttgg 720
gggtggttgg caagtacgcg acaaagagg gtagtgcgca aggaagcgag ttggatgcaa 780
ataatattac aaagtgggtt ggtgggcatg agcatcaacc agaatgatgt tgttgctggt 840
tccgtgcaaa ttctgaccag tagtttgaac aatactacc aacttgtttt tggtaaaaca 900
tgaagtgggt aaggagaatt gaacttacgt ctcatggtaa agggcaaggg caaatgactt 960
aacacatacc tttaactaat aaaaatacc ctaacaaata cgaaaacgaa tgagttatca 1020
cagacctca actaataaga tagccatcag accacatct cctgactgac caaaaacaaa 1080
tgacttcaac caactaagat acccatcaaa gctaaccac aaccaattc ctacttccc 1140
cttaccagac caaccaagca gacctacgc attaactact ttaggacgtg ggaattggg 1200
gtgccaccgt tgaagaatgg cactcagggt tggtaatccc tccacgtgta tgtagcagtc 1260
gtttggtgga gacggcgtgt ttgaatgtcc accttcagt ttggagaaca aggaaattgg 1320

Fig. 8A

SEQ ID 9

gcttatatta ggectggatc tcttgtttca gagcaggagt agttcaggac aggaactagc 1380
attcaagaat tcaattgccc tgccctgctc tgctctgctt tgctcaactt attgatccct 1440
gctctggttt gttcaatttc ttgaccctg ctgggttctg ctctggtttg cacactttct 1500
cgattatata agtcattttg gatccttgca aggaagagaa tatg 1544

Fig. 8B



Lanes 1-4: PCR amplification of Sweetgum P450-1 gene from control and transgenic loblolly pine cell lines. Note the 600 bp amplified fragment in lanes 2-4.

Lanes 6-9: PCR amplification of Hygromycin gene from control and transgenic loblolly pine cell lines. Note the 1000 bp amplified fragment in lanes 7-9.

Lane 1: Control PT52 line

Lane 2: Transgenic line Y2

Lane 3: Transgenic line Y17

Lane 4: Control plasmid pSSLsP450-1-impl-s

Lane 5: DNA size marker Phi 174/HaeII (BRL); top 4 bands indicate molecular size of 1354, 1078, 872 and 603 bp.

Lane 6: Control PT52 line

Lane 7: Transgenic line Y7

Lane 8: Transgenic line O4

Lane 9: Control plasmid pHygro

FIG. 9